

002027" 8662E/60

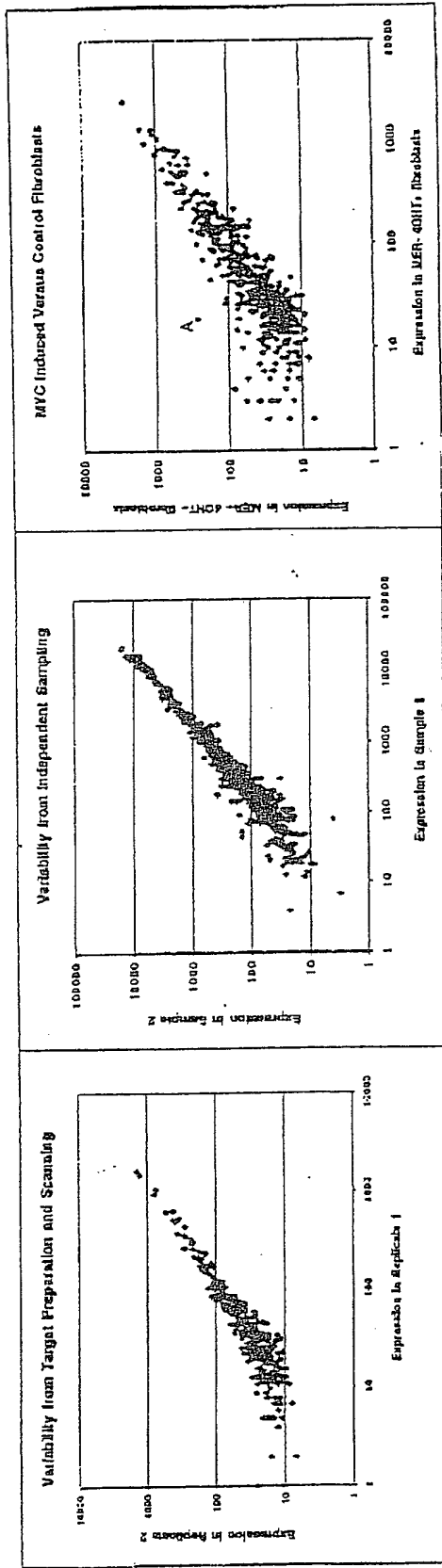


Figure 1A

Figure 1B

Figure 1C

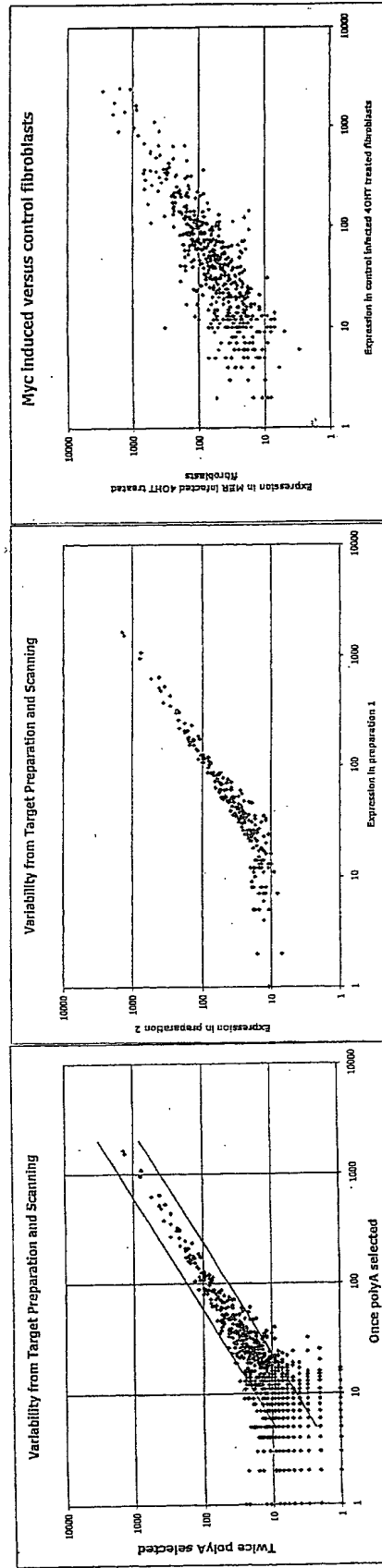


Figure 1D

Figure 1E

Figure 1F

002021" 8662E/60

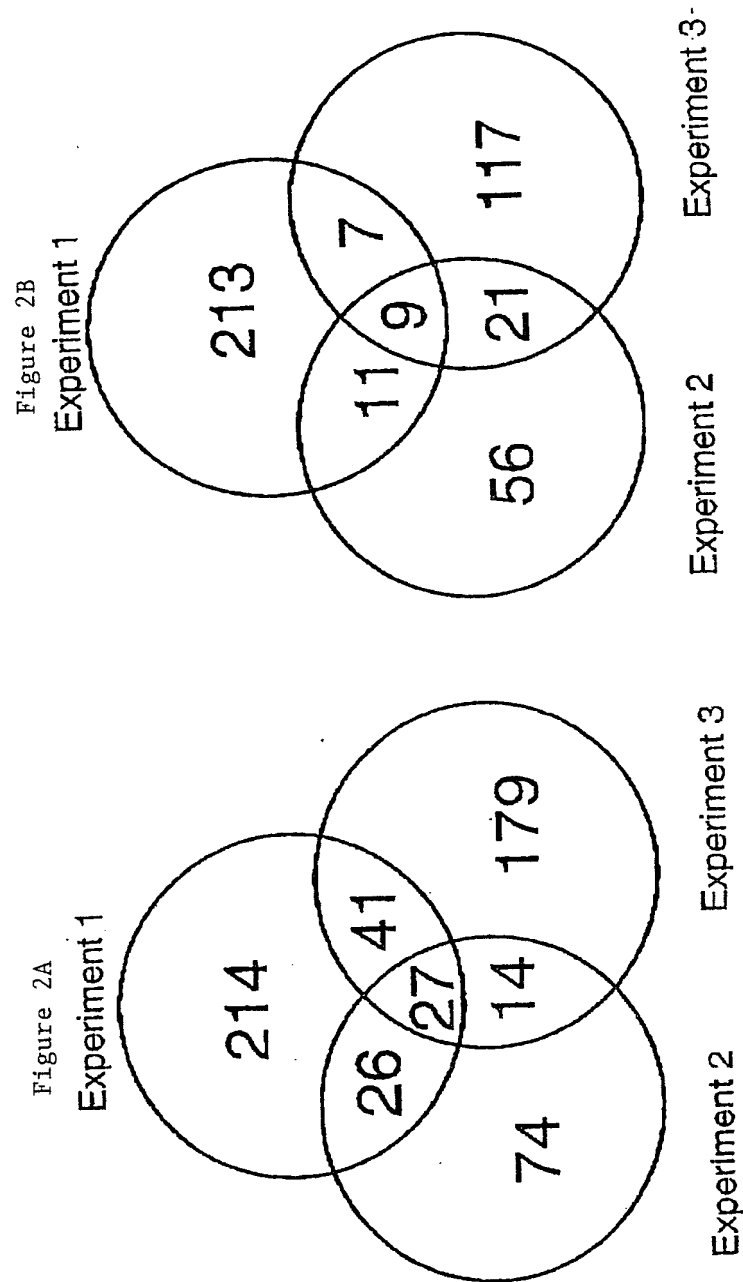


Figure 3A

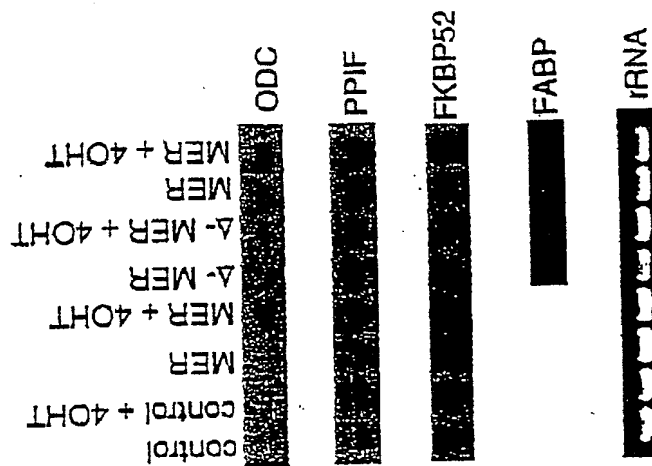


Figure 3B

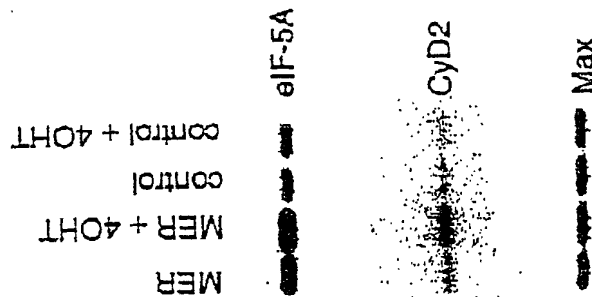
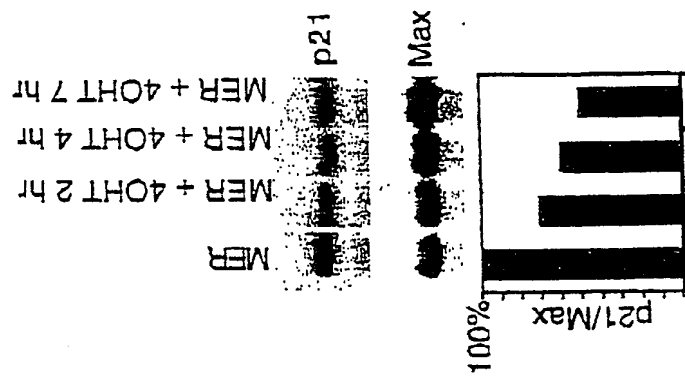
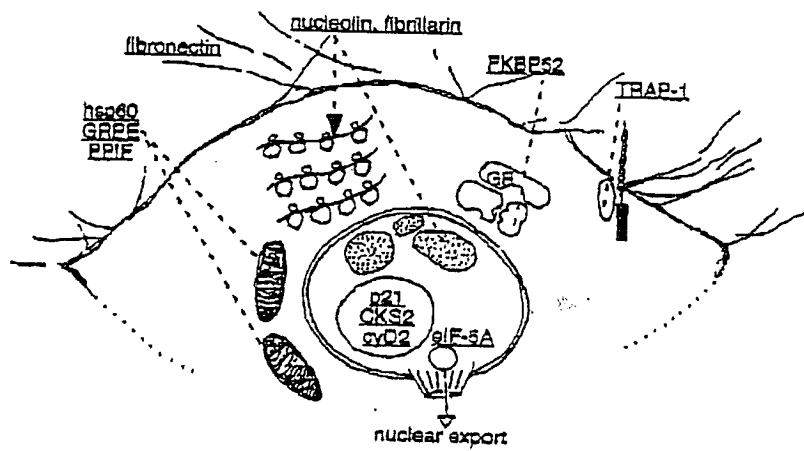


Figure 3C



00/021"86622600

Figure 4

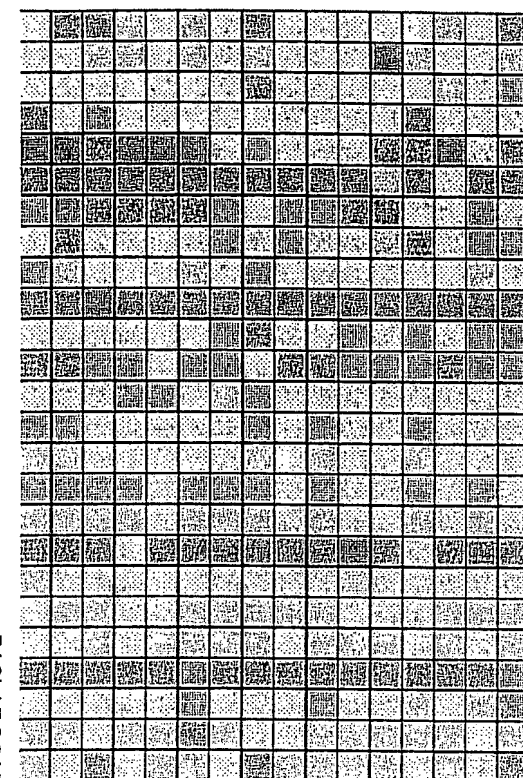


09732998-120700

004021" 36628260

Figure 5

MER1 MER2 MER3 Myc HL60 U937 NB4  
 MER/myc - - - + + - - - + + - - - +  
 4OHT - - - + + - - - + + - - - +  
 hours 0.5 4 24 0.5 4 24 0.5 24 48 72



Reference  
 FKBP, 59 kDa  
 Inosine monophosphate dehydrogenase  
 Transcription factor AP-4  
 Set protooncogene  
 Tumor necrosis factor receptor associated TRAP1  
 RNA polymerase II subunit hRPB17  
 2G4, 38 kDa  
 Ubiquinol cytochrome c reductase  
 Mitochondrial heat shock 60 kDa protein  
 HLA DR associated protein  
 Grpe protein homolog  
 Cyclin D2  
 S-adenosylhomocysteine hydrolase  
 Mitochondrial outer membrane protein  
 Mitochondrial acetoacetyl-CoA thiolase

Figure 6

Induced genes	Accession Number	MYC-ER1 MYC-ER + OHT/ control + OHT	MYC-ER2 MYC-ER + OHT/ control + OHT	MYC-ER3 MYC-ER + OHT/ control + OHT	Cycloheximide MYC-ER + OHT + $\alpha$ / control + OHT + $\alpha$	HL60 0 hr/24 hr
Ornithine decarboxylase 1*	X55362	5.0	5.2	7.5	2.5	3.1
AHCY, S-adenosylhomocysteine hydrolase*	M61832	2.3	2.4	7.3	6.8	3.4
CCND2, cyclin D2*	D13639	4.8	2.2	5.7	4.4	5.6
ASS, argininosuccinate synthetase*	T51288	2.7	2.1	5.5	2.9	0.5
FKBP52, 52-kDa FK506 binding protein*	T70920	14.7	4.3	5.4	2.4	4.2
Pre-B cell enhancing factor (PBEF)	U02020	2.5	4.0	5.2	1.9	0.4
Tumor necrosis factor receptor associated protein (TRAP1)*	R61502	4.3	4.5	5.0	2.8	2.9
FABP5, psoriasis-associated fatty acid binding protein*	H73758	8.3	13.6	4.7	2.7	10.0
Nucleolin*	H17434	2.4	2.7	4.5	4.0	2.2
GOS2, lymphocyte G0/G1 switch gene 2*	M69199	7.3	4.0	4.4	6.1	1.0
PIF (hCyp3), peptidyl-prolyl <i>cis-trans</i> isomerase F*	H55916	3.8	3.9	4.3	3.6	0.7
RNA polymerase II subunit (hsRPB8)	Z49199	2.8	2.4	4.0	1.4	1.3
Fibrillarin*	T57468	3.9	4.4	3.9	3.5	2.0
TFR, transferrin receptor (p90, CD71)*	R23889	2.3	2.4	3.9	2.4	9.1
CksHs2*	X54942	2.4	2.1	3.3	3.7	3.2
SLC16A1, solute carrier family 16*	L31801	11.1	2.7	2.9	2.0	5.6
IARS, isoleucine-tRNA synthetase*	U04953	5.9	2.1	2.9	2.6	1.3
HLA-DRB1, major histocompatibility complex, DR beta 5	T62633	3.4	8.9	2.9	0.4	0.5
EST highly similar to GRPE protein homolog precursor*	T51856	9.7	3.1	2.8	2.0	7.1
GPI, glucose phosphate isomerase	R49964	3.1	2.5	2.7	1.6	0.5
HSPD1, heat shock 60-kD protein 1 (chaperonin)	M22382	2.7	2.3	2.7	1.8	2.2
Hepatoma-derived growth factor*	D16431	2.2	2.3	2.6	2.6	2.5
Splicing factor SF2	R60749	4.3	3.6	2.5	1.6	6.3
Coup transcription factor	M37197	3.2	2.9	2.5	1.1	2.4
RP511, ribosomal protein S11	X60673	7.3	2.6	2.4	1.6	1.3
EIF5A, eukaryotic translation initiation factor 5A*	M23419	3.0	2.3	2.3	2.3	4.8
EIF4G, eukaryotic translation initiation factor 4 gamma	R39681	2.4	3.8	2.1	0.7	1.1
Repressed genes						
p311 (neuronal protein 3.1)*	U30521	0.29	0.38	0.15	0.13	0.43
A2M, alpha-2-macroglobulin*	T69425	0.10	0.22	0.18	0.22	0.22
TPM1, tropomyosin alpha chain (skeletal muscle)*	Z24727	0.33	0.31	0.20	0.14	1.10
PDGFRA, platelet-derived growth factor receptor alpha*	H23235	0.43	0.30	0.30	0.42	1.00
FN1, fibronectin 1*	M76378	0.48	0.39	0.30	0.35	0.53
CTGF, connective tissue growth factor*	X78947	0.32	0.33	0.31	0.24	1.00
COL3A1, alpha-1 type 3 collagen*	X06700	0.34	0.38	0.39	0.33	1.00
CDKN1A, cyclin-dependent kinase inhibitor 1A (p21, Cip1)*	U03106	0.24	0.48	0.41	0.33	0.04
EST moderately similar to dithiolethione-inducible gene-2	R73450	0.22	0.38	0.44	0.93	0.28

Genes are listed in order of fold induction in experiment 3. The following genes were not present on the microarrays: EIF2a, CAD, ECA-39, MrDb, telomerase, LAF-1a, HLA-A2, gadd45, C/EBP $\alpha$ , and iron regulatory protein 2.

\*Regulated by MYC-ER in the presence of cycloheximide.